

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING ERROR REPORT**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:**

Application Serial Number: 101573.130  
Source: TELUK  
Date Processed by STIC: 9-4-06

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>10/573,130</u>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input type="checkbox"/> Wrapped Nucleics <input type="checkbox"/> Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor <b>after</b> creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line <b>not exceed</b> 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. <b>Do not use tab codes between numbers; use space characters</b> , instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was <b>not saved</b> in ASCII(DOS) text, as <b>required</b> by the Sequence Rules. <b>Please ensure your subsequent submission is saved in ASCII text.</b>	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. <b>Per Sequence Rules, each n or Xaa can only represent a single residue.</b> Please present the <b>maximum</b> number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. <b>This applies to the mandatory &lt;220&gt;-&lt;223&gt; sections for Artificial or Unknown sequences.</b>	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for <b>each</b> skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to <b>include</b> the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If <b>intentional</b> , please insert the following lines for <b>each</b> skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is <b>MANDATORY</b> if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the <b>only valid</b> <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is <b>required</b> when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is <b>MANDATORY</b> if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input checked="" type="checkbox"/> Misuse of n/Xaa	"n" can <b>only</b> represent a single <u>nucleotide</u> ; "Xaa" can <b>only</b> represent a single <u>amino acid</u>	



IFWP

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/573,130

DATE: 04/04/2006

TIME: 10:13:06

Input Set : A:\Final Sequence list-13111-00035-US.txt  
 Output Set: N:\CRF4\04042006\J573130.raw

3 <110> APPLICANT: Sturmer, Rainer  
 4       Kesseler, Maria  
 5       Hauer, Bernhard  
 6       Friedrich, Thomas  
 7       Breuer, Michael  
 9 <120> TITLE OF INVENTION: Methods for the production of  
 10      3-methylamino-1-(thiene-2-yl)-propane-1-ol  
 12 <130> FILE REFERENCE: 13111-00035-US  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/573,130  
 C--> 14 <141> CURRENT FILING DATE: 2006-03-23  
 14 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/010939  
 15 <151> PRIOR FILING DATE: 2004-09-30  
 17 <150> PRIOR APPLICATION NUMBER: DE 103 45 772.0  
 18 <151> PRIOR FILING DATE: 2003-10-01  
 20 <160> NUMBER OF SEQ ID NOS: 44  
 22 <170> SOFTWARE: PatentIn version 3.3  
 26 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 47  
 30 <212> TYPE: PRT  
 32 <213> ORGANISM: Lactobacillus brevis  
 36 <400> SEQUENCE: 1  
 38 Met Ser Asn Arg Leu Asp Gly Lys Val Ala Ile Val Thr Gly Thr  
 39               5                   10                   15  
 42 Leu Gly Ile Gly Leu Ala Ile Ala Thr Lys Phe Val Glu Glu Gly Ala  
 43               20               25                   30  
 46 Lys Val Met Ile Thr Gly Arg His Ser Asp Val Gly Glu Lys Ala  
 47               35               40                   45  
 50 <210> SEQ ID NO: 2  
 52 <211> LENGTH: 18  
 54 <212> TYPE: PRT  
 56 <213> ORGANISM: Candida magnoliae  
 60 <400> SEQUENCE: 2  
 62 Ser Asn Ala Leu Val Thr Gly Ser Arg Val Ile Gly Ala Gly Gly  
 63               1               5                   10                   15  
 66 Phe Ile  
 70 <210> SEQ ID NO: 3  
 72 <211> LENGTH: 756  
 74 <212> TYPE: DNA  
 76 <213> ORGANISM: Lactobacillus brevis  
 80 <220> FEATURE:  
 82 <221> NAME/KEY: CDS  
 84 <222> LOCATION: (1)..(756)  
 88 <400> SEQUENCE: 3

(pg.7)

Does Not Contain

Corrected Diskette Needed

(pg.6)

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/10/573,130**

**DATE: 04/04/2006**  
**TIME: 10:13:06**

**Input Set : A:\Final Sequence list-13111-00035-US.txt**  
**Output Set: N:\CRF4\04042006\J573130.raw**

89 atg tct aac cgt ttg gat gga aaa gta gca atc gtt aca ggt ggt acg	48
90 Met Ser Asn Arg Leu Asp Gly Lys Val Ala Ile Val Thr Gly Gly Thr	
91 1 5 10 15	
93 ttg ggt atc ggt tta gct atc gcc acg aag ttc gtt gaa gaa ggg gct	96
94 Leu Gly Ile Gly Leu Ala Ile Ala Thr Lys Phe Val Glu Glu Gly Ala	
95 20 25 30	
97 aag gtc atg att acc ggc cggt cac agc gat gtt ggt gaa aaa gca gct	144
98 Lys Val Met Ile Thr Gly Arg His Ser Asp Val Gly Glu Lys Ala Ala	
99 35 40 45	
101 aag agt gtc ggc act cct gat cag att caa ttt ttc caa cat gat tct	192
102 Lys Ser Val Gly Thr Pro Asp Gln Ile Gln Phe Phe Gln His Asp Ser	
103 50 55 60	
105 tcc gat gaa gac ggc tgg acg aaa tta ttc gat gca acg gaa aaa gcc	240
106 Ser Asp Glu Asp Gly Trp Thr Lys Leu Phe Asp Ala Thr Glu Lys Ala	
107 65 70 75 80	
109 ttt ggc cca gtt tct aca tta gtt aat aac gct ggg atc gcg gtt aac	288
110 Phe Gly Pro Val Ser Thr Leu Val Asn Asn Ala Gly Ile Ala Val Asn	
111 85 90 95	
113 aag agt gtc gaa gaa acc acg att gct gaa tgg cgt aaa cta tta gcc	336
114 Lys Ser Val Glu Glu Thr Thr Ala Glu Trp Arg Lys Leu Leu Ala	
115 100 105 110	
117 gtc aac ctt gat ggt gtc ttc ggt acc cga tta ggg att caa cgg	384
118 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg	
119 115 120 125	
121 atg aag aac aaa ggc tta ggg gct tcc atc atc aac atg tct tcg atc	432
122 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile	
123 130 135 140	
125 gaa ggc ttt gtg ggt gat cct agc tta ggg gct tac aac gca tct aaa	480
126 Glu Gly Phe Val Gly Asp Pro Ser Leu Gly Ala Tyr Asn Ala Ser Lys	
127 145 150 155 160	
129 ggg gcc gta cgg att atg tcc aag tca gct gcc tta gat tgt gcc cta	528
130 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu	
131 165 170 175	
133 aag gac tac gat gtt cgg gta aac act gtt cac cct gcc tac atc aag	576
134 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Tyr Ile Lys	
135 180 185 190	
137 aca cca ttg gtt gat gac cta cca ggg gcc gaa gaa gcg atg tca caa	624
138 Thr Pro Leu Val Asp Asp Leu Pro Gly Ala Glu Ala Met Ser Gln	
139 195 200 205	
141 cgg acc aag acg cca atg ggc cat atc ggt gaa cct aac gat att gcc	672
142 Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala	
143 210 215 220	
145 tac atc tgt gtt tac ttg gct tct aac gaa tct aaa ttt gca acg ggt	720
146 Tyr Ile Cys Val Tyr Leu Ala Ser Asn Glu Ser Lys Phe Ala Thr Gly	
147 225 230 235 240	
149 tct gaa ttt gta gtt gac ggt ggc tac act gct caa	756
150 Ser Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln	
151 245 250	
154 <210> SEQ ID NO: 4	

**RAW SEQUENCE LISTING** DATE: 04/04/2006  
 PATENT APPLICATION: US/10/573,130 TIME: 10:13:06

Input Set : A:\Final Sequence list-13111-00035-US.txt  
 Output Set: N:\CRF4\04042006\J573130.raw

```

156 <211> LENGTH: 252
158 <212> TYPE: PRT
160 <213> ORGANISM: Lactobacillus brevis
164 <400> SEQUENCE: 4
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167 1 5 10 15
170 Leu Gly Ile Gly Leu Ala Ile Ala Thr Lys Phe Val Glu Glu Gly Ala
171 20 25 30
174 Lys Val Met Ile Thr Gly Arg His Ser Asp Val Gly Glu Lys Ala Ala
175 35 40 45
178 Lys Ser Val Gly Thr Pro Asp Gln Ile Gln Phe Phe Gln His Asp Ser
179 50 55 60
182 Ser Asp Glu Asp Gly Trp Thr Lys Leu Phe Asp Ala Thr Glu Lys Ala
183 65 70 75 80
186 Phe Gly Pro Val Ser Thr Leu Val Asn Asn Ala Gly Ile Ala Val Asn
187 85 90 95
190 Lys Ser Val Glu Glu Thr Thr Ala Glu Trp Arg Lys Leu Leu Ala
191 100 105 110
194 Val Asn Leu Asp Gly Val Phe Phe Gly Thr Arg Leu Gly Ile Gln Arg
195 115 120 125
198 Met Lys Asn Lys Gly Leu Gly Ala Ser Ile Ile Asn Met Ser Ser Ile
199 130 135 140
202 Glu Gly Phe Val Gly Asp Pro Ser Leu Gly Ala Tyr Asn Ala Ser Lys
203 145 150 155 160
206 Gly Ala Val Arg Ile Met Ser Lys Ser Ala Ala Leu Asp Cys Ala Leu
207 165 170 175
210 Lys Asp Tyr Asp Val Arg Val Asn Thr Val His Pro Gly Tyr Ile Lys
211 180 185 190
214 Thr Pro Leu Val Asp Asp Leu Pro Gly Ala Glu Glu Ala Met Ser Gln
215 195 200 205
218 Arg Thr Lys Thr Pro Met Gly His Ile Gly Glu Pro Asn Asp Ile Ala
219 210 215 220
222 Tyr Ile Cys Val Tyr Leu Ala Ser Asn Glu Ser Lys Phe Ala Thr Gly
223 225 230 235 240
226 Ser Glu Phe Val Val Asp Gly Gly Tyr Thr Ala Gln
227 245 250
230 <210> SEQ ID NO: 5
232 <211> LENGTH: 472
234 <212> TYPE: DNA
236 <213> ORGANISM: Candida magnoliae
240 <220> FEATURE:
242 <221> NAME/KEY: CDS
244 <222> LOCATION: (1)..(471)
248 <400> SEQUENCE: 5
249 aac gcg ctg gtg acg ggc ggc agc cgc ggc att ggc gaa gcc act gcc 48
250 Asn Ala Leu Val Thr Gly Gly Ser Arg Gly Ile Gly Glu Ala Thr Ala
251 1 5 10 15
253 att aag ctc gcc gag gag ggc tac agc gtc acg att gcg tct cgc ggc 96
254 Ile Lys Leu Ala Glu Glu Gly Tyr Ser Val Thr Ile Ala Ser Arg Gly
  
```

**RAW SEQUENCE LISTING** DATE: 04/04/2006  
**PATENT APPLICATION:** US/10/573,130 TIME: 10:13:06

Input Set : A:\Final Sequence list-13111-00035-US.txt  
Output Set: N:\CRF4\04042006\J573130.raw

255	20	25	30	
257	c当地 aag cag ctc gag gct gtg aag gcc aaa cta ccc att gtg aag cag			144
258	Leu Lys Gln Leu Glu Ala Val Lys Ala Lys Leu Pro Ile Val Lys Gln			
259	35	40	45	
261	gga cag gtt cac cac gtg tgg cag ctt gat ctc agt gat gtc gac gct			192
262	Gly Gln Val His His Val Trp Gln Leu Asp Leu Ser Asp Val Asp Ala			
263	50	55	60	
265	gcg gcc gcc ttc aaa ggg tcg ccg cta cct gcc agc cgc tac gac gtg			240
266	Ala Ala Ala Phe Lys Gly Ser Pro Leu Pro Ala Ser Arg Tyr Asp Val			
267	65	70	75	80
269	ctc gtc agc aat gct ggc gtg gcc cag ttt agc ccg ttc atc gag cat			288
270	Leu Val Ser Asn Ala Gly Val Ala Gln Phe Ser Pro Phe Ile Glu His			
271	85	90	95	
273	gcg aag cag gac tgg tcg cag atg ctt gcc atc aat ctg gcg gca ccc			336
274	Ala Lys Gln Asp Trp Ser Gln Met Leu Ala Ile Asn Leu Ala Ala Pro			
275	100	105	110	
277	att gcg ctg gcc cag aca ttt gct aag gcc att ggc gac aag ccg cgc			384
278	Ile Ala Leu Ala Gln Thr Phe Ala Lys Ala Ile Gly Asp Lys Pro Arg			
279	115	120	125	
281	aac aca cgg gcc cac att gtg ttt gtc tcg tcg aac gtc tcg tgg cga			432
282	Asn Thr Pro Ala His Ile Val Phe Val Ser Ser Asn Val Ser Leu Arg			
283	130	135	140	
285	ggc ttc ccg aac atc ggc gtc aac tcc atc acc ccc ggc a			472
286	Gly Phe Pro Asn Ile Gly Val Asn Ser Ile Thr Pro Gly			
287	145	150	155	
290	<210> SEQ ID NO: 6			
292	<211> LENGTH: 157			
294	<212> TYPE: PRT			
296	<213> ORGANISM: Candida magnoliae			
300	<400> SEQUENCE: 6			
302	Asn Ala Leu Val Thr Gly Gly Ser Arg Gly Ile Gly Glu Ala Thr Ala			
303	1	5	10	15
306	Ile Lys Leu Ala Glu Glu Gly Tyr Ser Val Thr Ile Ala Ser Arg Gly			
307	20	25	30	
310	Leu Lys Gln Leu Glu Ala Val Lys Ala Lys Leu Pro Ile Val Lys Gln			
311	35	40	45	
314	Gly Gln Val His His Val Trp Gln Leu Asp Leu Ser Asp Val Asp Ala			
315	50	55	60	
318	Ala Ala Ala Phe Lys Gly Ser Pro Leu Pro Ala Ser Arg Tyr Asp Val			
319	65	70	75	80
322	Leu Val Ser Asn Ala Gly Val Ala Gln Phe Ser Pro Phe Ile Glu His			
323	85	90	95	
326	Ala Lys Gln Asp Trp Ser Gln Met Leu Ala Ile Asn Leu Ala Ala Pro			
327	100	105	110	
330	Ile Ala Leu Ala Gln Thr Phe Ala Lys Ala Ile Gly Asp Lys Pro Arg			
331	115	120	125	
334	Asn Thr Pro Ala His Ile Val Phe Val Ser Ser Asn Val Ser Leu Arg			
335	130	135	140	
338	Gly Phe Pro Asn Ile Gly Val Asn Ser Ile Thr Pro Gly			

RAW SEQUENCE LISTING DATE: 04/04/2006  
PATENT APPLICATION: US/10/573,130 TIME: 10:13:06

Input Set : A:\Final Sequence list-13111-00035-US.txt  
Output Set: N:\CRF4\04042006\J573130.raw

339 145 150 155  
343 <210> SEQ ID NO: 7  
344 <211> LENGTH: 27  
345 <212> TYPE: DNA  
346 <213> ORGANISM: Artificial sequence  
348 <220> FEATURE:  
349 <223> OTHER INFORMATION: Primer: Mke 338  
351 <400> SEQUENCE: 7  
352 ggaaattcca tatgtctaac cgtttgg 27  
355 <210> SEQ ID NO: 8  
356 <211> LENGTH: 28  
357 <212> TYPE: DNA  
358 <213> ORGANISM: Artificial sequence  
360 <220> FEATURE:  
361 <223> OTHER INFORMATION: Primer: Mke 339  
363 <400> SEQUENCE: 8  
364 ctagggaag cttattgagc agtgttagc 28  
367 <210> SEQ ID NO: 9  
368 <211> LENGTH: 28  
369 <212> TYPE: DNA  
370 <213> ORGANISM: Artificial sequence  
372 <220> FEATURE:  
373 <223> OTHER INFORMATION: Primer: Mke 366  
375 <400> SEQUENCE: 9  
376 acgacgacga gcaacgcgt bgtbacgg 28  
379 <210> SEQ ID NO: 10  
380 <211> LENGTH: 28  
381 <212> TYPE: DNA  
382 <213> ORGANISM: Artificial sequence  
384 <220> FEATURE:  
385 <223> OTHER INFORMATION: Primer: Mke 367  
387 <400> SEQUENCE: 10  
388 acgacgacgt cgaacgcgt bgtbacgg 28  
391 <210> SEQ ID NO: 11  
392 <211> LENGTH: 27  
393 <212> TYPE: DNA  
394 <213> ORGANISM: Artificial sequence  
396 <220> FEATURE:  
397 <223> OTHER INFORMATION: Primer: Mke 374  
399 <400> SEQUENCE: 11  
400 gccggggttt atsswgttsa cgccgat 27  
403 <210> SEQ ID NO: 12  
404 <211> LENGTH: 10  
405 <212> TYPE: PRT  
406 <213> ORGANISM: Lactobacillus brevis  
409 <220> FEATURE:  
410 <221> NAME/KEY: MISC\_FEATURE  
411 <222> LOCATION: (1)..(10)  
412 <223> OTHER INFORMATION: Fragment: C terminus

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Page 6

<210> 15  
<211> 60  
<212> PRT  
<213> Lactobacillus brevis

<220>  
<221> VARIANT  
<222> (47)..(47)  
<223> Amino acid is Ala or Lys

<220>  
<221> UNSURE  
<222> (48)..(48)  
<223> Amino acid is Lys or Ala

<220>  
<221> VARIANT  
<222> (53)..(53)  
<223> Amino acid is Pro or Thr

<220>  
<221> VARIANT  
<222> (59)..(59)  
<223> Amino acid is Phe, Val, Gly, or Asn

<220>  
<221> misc\_feature  
<222> (60)..(60)  
<223> Xaa is unreadable

<400> 15

*INVALID response?*  
*do you mean?*  
*UNKNOWN?*

*See item*

*# 13*

*on error summary sheet.*

Ser Asn Arg Leu Asp Gly Lys Val Ala Ile Val Thr Gly Gly Thr Leu  
1 5 10 15

Gly Ile Gly Leu Ala Ile Ala Thr Lys Phe Val Glu Glu Gly Ala Lys  
20 25 30

Val Met Ile Thr Gly Arg His Ser Asp Val Gly Glu Lys Ala Ala Lys  
35 40 45

Ser Val Gly Thr Pro Asp Gln Ile Gln Phe Phe Xaa

*pls explain "Xaa"*  
*=*  
*location.*

FYI:

"Xaa" can only  
represent a  
single amino  
acid.

The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 04/04/2006  
PATENT APPLICATION: US/10/573,130 TIME: 10:13:07

Input Set : A:\Final Sequence list-13111-00035-US.txt  
Output Set: N:\CRF4\04042006\J573130.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:15; Xaa Pos. 60  
Seq#:16; Xaa Pos. 19,20  
Seq#:17; Xaa Pos. 12,13,14,15  
Seq#:18; Xaa Pos. 8  
Seq#:19; Xaa Pos. 9,11,12,13,14,15  
Seq#:22; Xaa Pos. 6,10,11,12,13,14,15  
Seq#:23; Xaa Pos. 6,12,15,16,17,18  
Seq#:24; Xaa Pos. 6,10,11,12,13,14,15,16,17  
Seq#:25; Xaa Pos. 16,17,18,19,20  
Seq#:26; Xaa Pos. 1,3  
Seq#:27; Xaa Pos. 9,13  
Seq#:28; Xaa Pos. 7,17,18,19,20  
Seq#:30; Xaa Pos. 1,10,11,12,13,14,15,16,17,18,19,20  
Seq#:32; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20  
Seq#:33; Xaa Pos. 5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20  
Seq#:34; Xaa Pos. 3,13,14,15,16,17,18,19,20  
Seq#:35; Xaa Pos. 11,12,13,14  
Seq#:36; Xaa Pos. 1  
Seq#:40; Xaa Pos. 1  
Seq#:41; Xaa Pos. 2,39,40  
Seq#:42; Xaa Pos. 37,38,39  
Seq#:43; Xaa Pos. 12,13,14,15  
Seq#:44; Xaa Pos. 13,14,15

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/573,130

DATE: 04/04/2006

TIME: 10:13:07

Input Set : A:\Final Sequence list-13111-00035-US.txt  
Output Set: N:\CRF4\04042006\J573130.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:502 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:48  
L:602 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:16  
L:623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0  
L:640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0  
L:711 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0  
L:806 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0  
L:903 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0  
L:907 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:16  
L:929 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0  
L:933 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:16  
L:950 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0  
L:954 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:16  
L:976 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0  
L:1063 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0  
L:1160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0  
L:1164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:16  
L:1326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0  
L:1330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:16  
L:1560 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:16  
L:1577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0  
L:1638 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0  
L:1642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:16  
L:1659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0  
L:1691 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0  
L:1821 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:0  
L:1851 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:0  
L:1859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:32  
L:1993 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:32  
L:2010 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0  
L:2072 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0